## Appendix III

Alignment of SEQ ID NO: 1479 of Tang et al with the sequence of GenBank Accession No. BAA23691.2

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Score = 1827 bits (4732), Expect = 0.0, Method: Compositional matrix adjust. Identities = 877/879 (998), Positives = 878/879 (998), Gaps = 0/879 (0%)			
Query	78	SCKYCDFRSHDMTQFVGHMMSEHTDFNKDPTFVCSGCSFLAKTFEGLSLHNATCHSGEAS SCKYCDFRSHDMTQFVGHMMSEHTDFNKDPTFVCSGCSFLAKTFEGLSLHNATCHSGEAS	137
Shjet	ī	SCKYCDFRSHDMTQFYGHMMSEHTDFMKDFTFYCSGCSFLAKKTFEGLSLHMATCHSGEAS	60
Query	138	fvwnvakfdnrvvveqsipeststrdlagefsaegadgqaeiiitktfimkinkgkaeak fvwnvakpdmrvvvegsipeststrdlagefsaegadggaeiiitktpimkinkgkaeak	197
Shjet	61	PYWWYARPDWHYYYEQSIPESTSTPDLAGEPSAEGADGQAEIIITKTPIMKIMKGKAEAK	120
Query	198	KIHTLKENVPSQPYGEALPKLSTGEMEYREGDHSFINGAVFVSQASASSAKNPHAANGEL KIHTLKENVPSQPYGEALPKLSTGEMEVREGDHSFINGAVPVSQASASSAKNPHAANGEL	257
Shjet	121	KIHTLKENYPSQPYGEALFKLSTGEMEVPEGDHSFINGAYPYSQASASSAKUPHAANGFL	180
Query	258	IGTVFVLPAGIAQFLSLQQQPFVHAQHHVHQFLPTAKALPKVMIPLSSIPTISAAMDSRS IGTVFVLPAGIAQFLSLQQQPFVHAQHHVHOFLPTAKALPKVMIFLSSIFTX+AAMDSRS	317
Sbjet	181	IGTVFVLPAGIAQFLSLQQQPPVHAQHHVHQPLPTAKALPKVMIPLSSIPTYNAAMDSNS	240
Query	318	elknsfhkepyptkaelcyltvvtkypeeqlkiwptaqelkqgiswspeeiedapkkmfn plknsfhkepyptkaelcyltvvtkypeeqlktwptaqelkqgiswspeeiedarkkmpn	377
Sbjct	241	FLKMSFHKFPYPTKAELCYLTVVTKYPEEQLKIWFTAOPLKOGISWSPEEIRDARKKMFN	300
Query	378	TVIQSVPQPTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEGTGGGLLVTQPLMAHGLQ TVIOSVPQPTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEGTGGGLLVTQPLMANGLQ	437
Sbjct	301	TVIQSVPQPTITVLNTPLVASAGNVQHLIQAALPGHVVGQPEGTGGGLLVTQPLMANGLQ	360
Query	438	ATSSPLPLTVTSVPKOPGVAPINTVCSNTTSAVKVVNAAQSLLTACPSITSQAFLDASIY ATSSPLPLTVTSVPKOPGVAPINTVCSNTTSAVKVVNAAQSLLTACPSITSOAFLDASIY	497
Sbjet	361	ATSSPERITYTSVFKQFGVAFINTVCSNTTSAVKVVNAAQSLETACPSITSQAFLDASIY	420
Query	498	KNKKSHEQLSALKGSPCPRQFPGQSEVEHLTKVTGLSTREVRKWFSDRFTHCRELKGSRA KNKKSHEGLSALKGSFCRROFPGGSEVEHLTKVTGLSTREVRKWFSDRRYHCRELKGSRA	557
Sbjct	421	KNEKSHEQLSALKGSTCREQFFQQSEVEHLTKVTGLSTREVRKWFSDRRYHCRELKGSRA	480
Query	558	MIPGDRSSIIIDSVPEVSFSPSSKVPEVTCIPTTATLATRPSAKROSWHQTPDFTFTKXK MIPGDRSSIIIDSVPEVSFSPSSKVPEVTCIPTTATLATRPSAKROSWHOTPDFTPTKXK	617
Sbjct	401	MIPGDHSSIIIDSVPEVSFSPSSKVPEVTCIPTTATLATHPSAKRQSWHQTPDPTFTKIK	540
Query	613	EPAPEQLRALESSFAQNFLPLDEELDRLRSETKMTRREIDSWFSERRKVNAFETKKAEE ERAPECLRALESSFAONFLPLDEELDRLRSETKMTREIDSWFSERRKVNAFETKKAEE	677
Sbjct	541	ERAPEQLRALESSFAQNP1PLDEELDRLRSETKMTRREIDSWFSERRKKVNAEETKKAEE	600
Query	678	NASQEEEEAAEDEGGEEDLASELRVSGENGSLEMPSSHILAERKVSPIKINLKMLRVTEA NASQEEEEAAEDEGGEEDLASELRVSGENGSLEMPSSHILAERKVSPIKINLKMLRVTEA	737
Sbjet	601	NASQEEEBAAEDEGGEEDLASELRVSGENGSLEMPSSHILAERKVSPIKINLKNLRVTEA	660
Query	738	ngrneipglgacdpeddesnklæglpgkvsckktagorhilrglfvotompsnodilsi ngrneipglgacdpeddesnklæglpgkvsckktagorhilrglfvotompsnodidsi	797
Shyet	661	NGRNEIPGLGACDPEDDESHKLAEQLPGKYSCKKTAQQRHLLRQLFVQTQWPSHQDYDSI	720
Query	798	MAQTGLPRPBVVPMFGDSRYALKHGQLKMYEDYKRGHFPPGLLVIAPGNPELLQDYYMTH MAQTGLPRPBVVRMFGDSRYALKHGQLKMYEDYKRGHFPPGLLVIAPGNRELLODYYMTH	857
Shjet	721	MAQTGLPRPEVYRMPGDSRYALKNGQLKWYEDYKRGNFFPGLLVIAPGNRELLQDYYNTH	780
Query	858	KMLYEEDLQMLCDKTQMSSQQVKQWFAEKMGEETRAVADTGSEDQGFGTGELTAVHKGMG KMLYEEDLOMLCDKTOMSSOOVKOWFAEKMGEETRAVADTGSEDQGFGT ELTAVHKGMG	917
Sbjet	781	MMLYEEDLQMLCDKTQMSSQQVKQWFAEKMGEETRAVADTGSEDQGFGTTELTAVHKGMG	840
Query	918	DTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD 956 DTYSEVSENSESWEPRVPEASSEPPDTSSPQAGRQLETD	
Sbjet	841	DTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD 879	